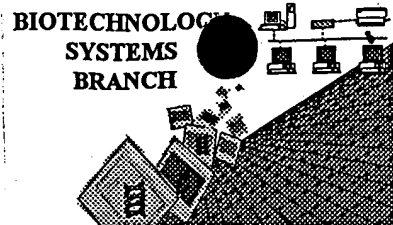


RAW SEQUENCE LISTING **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/088,384
Source: PCT 10
Date Processed by STIC: 4/10/02

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER**
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

PC T10

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/088,384

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 ✓ Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



Does Not Comply
Corrected Diskette Needed

PCT10

RAW SEQUENCE LISTING

DATE: 04/10/2002

PATENT APPLICATION: US/10/088,384

TIME: 12:58:26

Input Set : A:\31147.app

Output Set: N:\CRF3\04102002\J088384.raw

3 <110> APPLICANT: Syngenta Participations AG
6 <120> TITLE OF INVENTION: Transcriptionally Silenced Plant Genes
8 <130> FILE REFERENCE: S-31147A
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/088,384
C--> 11 <141> CURRENT FILING DATE: 2002-03-15
13 <150> PRIOR APPLICATION NUMBER: GB 9921964.4
14 <151> PRIOR FILING DATE: 1999-09-16
E--> 16 <160> NUMBER OF SEQ ID NOS: 26
18 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

228 <210> SEQ ID NO: 7
229 <211> LENGTH: 1956
230 <212> TYPE: DNA
231 <213> ORGANISM: Arabidopsis thaliana
233 <400> SEQUENCE: 7
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235 aatttgaaag aaaactgaac catgcctaga ttgctctact cgaccacact gtcattgatct 120
236 gataccattc cctatcaatt tgaacctgaa tttgatcttt aattatcatg tctgcatcaa 180
237 atttgaaactc atggataccc taaaataactt ggattttctt attcattttg atcaactcttg 240
238 ttaatccaag tagctgactc tccttattag agcagttaac ccgaacccaa acctagactt 300
239 tttttcaagc cttatatcac tcgtgagggg ttgtgaggtc ttattccgat tcagcttggt 360
E--> 240 agaaagtgtt aggttcgtaa cgacagagat agtgnctcat gtagttctag ttgcgatttt 420
E--> 241 ttggactaga taggactggg tgggcgctta tacttttaggt tgggatgngt ttaaaagaaa 480
242 aaaaaagggg ttgattcatt gatgagaaaa ggtaaaagac tctaggtgaa gtaagataaa 540
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247 gaggtaaagt cttatactgg gattggagat gggattacca ttagagcttc atctgatata 840
248 ctctaggtag atgggatctt atctctgcat gcatagtttg ggacttacct ttagcattct 900
249 actaaagctt aatcattttt tgagagatcc cctgttactg aagcctattc tgtaaggagc 960
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251 attcacgttc cagaactaat gaatgttaaa gggattggta gatttgaaaa catgtgtagg 1080
252 tcgagcatat gagtcggatt gattgatagt aaggcatggc taaagttttt cagtagaatt 1140
253 cgatcatatc gcagcttaga actatcaact tggacattga tttcattttg tttatctagt 1200
254 gctttggctc tgagtccccg atttcaaaac tcacctctag cttgttctta attgtttgct 1260
255 tgagggcaag caaagactaa gtttggggga gttgataagt gtgtattttg catgttttga 1320
256 gcatccattt gtcattcatt tagcaccata tcatcactat tttataccat ttctcatcat 1380
257 ttgtcatcac tttgcatggt taggatagtt ttgcatgcat gtggcatatt tgtgttggtt 1440
258 tcaagtgatt cggagctggt gaagaactaa ttggaagaag cggacctgat catgccaac 1500

*Not found in sequence
requires explanation
see error summary sheet item 9*

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/088,384

DATE: 04/10/2002

TIME: 12:58:26

Input Set : A:\31147.app

Output Set: N:\CRF3\04102002\J088384.raw

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259 cactcgacct caggtcgagt agacgcttca cgacctcaac acaccactcg accacctggt 1560
260 cgagtgtagg acttcaccac ttcacctcat cactcgaccc cctggccgag taccocacga 1620
261 gagtcactcg atcacttcac togaccccca ggctcgagtgt cttcacctcc accacctgac 1680
262 catcactcga tcacacgact ctacctggaa gtcgagtatc accatcacca cactcgact 1740
263 acatacttga tgtcgagctt cagagttctt tccattccgc actcaaccag aactcgagc 1800
264 acaaggaaaa aaagaagatt ctagcttatt actcgacctc tcaactcgacc acctgggtcg 1860
265 agtacagttc ttaatccgtc tcaatactgc gtcgttttga gtattagggt ttcggaatat 1920
266 ttttgcata agtagcacgt actttacatt ttcgag 1956

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405 <210> SEQ ID NO: 10

406 <211> LENGTH: 648

407 <212> TYPE: PRT

408 <213> ORGANISM: Arabidopsis thaliana

*Xaa found in sequence
- same error*

410 <400> SEQUENCE: 10

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414 Asp Glu Ala Glu Ser Trp Ser Thr Arg Pro Glu Arg Glu Gln Gln Ala
415             20             25             30
417 Tyr Glu Ser Phe Arg Ala Glu Thr Gln Arg Ser Val Ala Arg Arg Asn
418             35             40             45
420 Glu Arg Arg Ala Glu Ile Ala Arg Gly Lys Arg Ala Met Thr Ser Arg
421             50             55             60
423 Tyr Glu Leu Ile Asp Glu Asp Ile Asp Val Glu Tyr Glu Pro Glu Ser
424   65             70             75             80
426 Trp His Arg Glu Thr Lys Leu Leu Asn Lys Pro Asp Glu Val Thr Val
427             85             90             95
429 Glu Glu Tyr Ile Arg Leu Phe Glu Leu Asn Asp Phe Trp Gly Ala Arg
430             100            105            110
432 Tyr Pro Cys Tyr Glu Thr Leu Ala Gln Leu Arg Leu Leu Glu Asp Val
433             115            120            125
435 Gln His Leu Phe Glu Lys Cys His Leu Glu Thr Leu Met Ser Tyr Pro
436             130            135            140
438 Tyr Val Ala Tyr Lys Lys Glu Thr Ile Glu Phe Leu Ser Thr Leu Gln
439   145            150            155            160
441 Val Glu Leu Tyr Gln Gly Leu Thr Ala Asp Glu Leu Glu Ser Glu Gly
442             165            170            175
444 Leu Gly Phe Leu Thr Phe Ser Val Asn Glu Gln Arg Tyr Gln Leu Ser
445             180            185            190
447 Ile Lys Ser Leu Glu Gly Leu Phe Gly Phe Pro Ser Gly Lys Gly Thr
448             195            200            205
450 Lys Pro Lys Phe Glu Arg Glu Glu Leu Lys Asp Leu Trp Leu Thr Ile
451             210            215            220
453 Gly Asn Asp Leu Ala Leu Asn Ser Ala Arg Ser Lys Ser Asn Gln Ile
454   225            230            235            240
456 Arg Ser Pro Val Ile Arg Tyr Tyr Gln Arg Ser Val Ala Asn Val Leu
457             245            250            255
459 Tyr Pro Arg Glu Ser Thr Gly Thr Val Ser Asn Thr Asp Met Glu Met
460             260            265            270
462 Ile Asp Ser Ala Leu Lys Gly Ile Leu Arg Arg Thr Lys Gly Lys Lys
463             275            280            285

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/088,384

DATE: 04/10/2002

TIME: 12:58:26

Input Set : A:\31147.app

Output Set: N:\CRF3\04102002\J088384.raw

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465 Val Leu Lys Gly Asp Leu Asn Asp Thr Pro Pro Val Met Leu Leu Leu
466      290      295      300
468 Ile His Met Cys Gly Tyr Arg Lys Trp Ala His Thr Asn Gly Arg Lys
469 305      310      315      320
471 Lys Val Arg Gly Ala Leu Cys Val Gly Gly Val Val Thr Pro Ile Leu
472      325      330      335
474 Ile Ala Cys Gly Val Pro Leu Thr Ser Pro Gly Phe Asp Pro Arg Met
475      340      345      350
477 Met Asp Leu Asp His Leu Arg Arg Cys Glu Phe Leu Glu Tyr Asp Met
478      355      360      365
480 Val Gly Asp Phe Tyr Arg Tyr Lys Phe Glu His Ser Leu Thr Arg Thr
481      370      375      380
E--> 483 Ala Asn Ile Leu Leu Pro Cys Ile Glu Ala Thr Thr Ile Leu Xaa Gly
484 385      390      395      400
486 Glu Asn Ile Asp Phe Arg Pro Ala Arg Asp Tyr Leu Tyr Phe Glu Ser
487      405      410      415
489 Thr Pro Pro Thr Asp Asp Asn Val Pro Thr Thr Glu Ala Thr Glu Asp
490      420      425      430
492 Asp Phe Ala Glu Thr Asp Glu Asp Arg Glu Glu Glu Tyr Asp Thr Ser
493      435      440      445
495 Met Tyr His Phe Ser Glu His Val Pro Pro Ala Gln Glu Ser Lys Ser
496      450      455      460
498 Leu Ser Glu Ala His Arg Asn Asn Ser Lys Leu Gln Arg Trp Cys Lys
499 465      470      475      480
501 Lys Gln Asp Arg Leu Leu Ile Lys Cys Phe Lys Ala Ile Thr Phe Leu
502      485      490      495
504 Thr Asp Lys Ile Ser Cys Phe Ser Ser Thr Thr Ala Ile Pro Gln Gly
505      500      505      510
507 Glu Arg Pro Gln Asp Met Pro Ser Lys Arg Tyr Asp Ala Pro Gly Pro
508      515      520      525
510 Ser His His Arg Pro Glu Pro Ser His His Arg Pro Glu Pro Ser Asp
511      530      535      540
513 Arg Val Val Pro Pro Val Pro Ala Arg His Ser Ser Phe Glu Pro Arg
514 545      550      555      560
516 Glu Leu Gly Arg Lys Lys Lys Ala Ala Leu Ala Arg Ser Gly Ser Arg
517      565      570      575
519 Ser Arg Arg Leu Leu Gln Ser Arg Ser Leu Arg Asp Arg Gly Ala Gly
520      580      585      590
522 Arg Ser Arg Arg Arg Glu Val Glu Tyr His Gln Ser Gly Ala Gly Arg
523      595      600      605
525 Gly Glu Gly Ala Glu Val Glu Tyr Pro Gln Gly Glu Ala Glu Thr Gln
526      610      615      620
528 Gln Gly Asp Ser Ser Met Ala Trp Glu Gln Ser Gln Ala Ala Ile Asp
529 625      630      635      640
531 Asp Gln Leu Arg Ser Phe Phe His
532      645

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/088,384

DATE: 04/10/2002

TIME: 12:58:27

Input Set : A:\31147.app

Output Set: N:\CRF3\04102002\J088384.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:240 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:7
M:340 Repeated in SeqNo=7
L:483 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:10
L:16 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (26) Counted (27)